



SEQUENCE LISTING

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<110> Wilkins, Thea A.
The Regents of the University of California

<120> Cotton Transcription Factors and Their Uses

<130> 023070-095600US

<140> US 09/453,387

<141> 1999-12-02

<160> 26

<170> PatentIn Ver. 2.1

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<223> GhMYB1

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atg gga cga tca cct tgt tgt gaa aag gct cat acc aac aaa ggt gcc      106
Met Gly Arg Ser Pro Cys Cys Glu Lys Ala His Thr Asn Lys Gly Ala
  1             5             10             15

tgg acc aaa gag gaa gat caa cgc ctc atc aac tac atc cgt gtc cat      154
Trp Thr Lys Glu Glu Asp Gln Arg Leu Ile Asn Tyr Ile Arg Val His
             20             25             30

ggt gaa ggc tgc tgg cgt tcc ctc ccc aaa gct gct ggg ctg ctt aga      202
Gly Glu Gly Cys Trp Arg Ser Leu Pro Lys Ala Ala Gly Leu Leu Arg
             35             40             45

tgt ggt aag agt tgc aga tta aga tgg ata aac tac ttg agg cct gat      250
Cys Gly Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Pro Asp
             50             55             60

ctt aag aga gga aat ttc act gaa gaa gaa gat gag ctt atc atc aag      298
Leu Lys Arg Gly Asn Phe Thr Glu Glu Glu Asp Glu Leu Ile Ile Lys
             65             70             75             80

ctt cac agt tta ctt gga aac aaa tgg tca ttg att gct gga aga tta      346
Leu His Ser Leu Leu Gly Asn Lys Trp Ser Leu Ile Ala Gly Arg Leu
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cca gga aga aca gat aat gag ata aag aac tac tgg aac aca cac atc      394
Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Asn Thr His Ile
             100             105             110

aaa aga aag ctt ata agc aga gga att gat cca caa act cat cgt cct      442
Lys Arg Lys Leu Ile Ser Arg Gly Ile Asp Pro Gln Thr His Arg Pro
             115             120             125
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| ctc aat caa acg gcc aat acc aac aca gtc aca gcc ccc acc gaa ttg | 490 |
| Leu Asn Gln Thr Ala Asn Thr Asn Thr Val Thr Ala Pro Thr Glu Leu | |
| 130 135 140 | |
| gat ttc aga aac tcg ccc aca tcc gtt tcc aaa tcc agt tcc atc aaa | 538 |
| Asp Phe Arg Asn Ser Pro Thr Ser Val Ser Lys Ser Ser Ser Ile Lys | |
| 145 150 155 160 | |
| aac ccg tct ctg gat ttc aat tac aat gaa ttt caa ttc aag tcc aac | 586 |
| Asn Pro Ser Leu Asp Phe Asn Tyr Asn Glu Phe Gln Phe Lys Ser Asn | |
| 165 170 175 | |
| aca gat tcc ctt gaa gaa ccc aac tgt aca gcc agc agt ggc atg act | 634 |
| Thr Asp Ser Leu Glu Glu Pro Asn Cys Thr Ala Ser Ser Gly Met Thr | |
| 180 185 190 | |
| aca gat gaa gag caa caa gaa cag ctg cac aag aag cag caa tac ggt | 682 |
| Thr Asp Glu Glu Gln Gln Glu Gln Leu His Lys Lys Gln Gln Tyr Gly | |
| 195 200 205 | |
| ccg agc aat ggg caa gac ata aat ttg gag ctg tcg att ggg att gtt | 730 |
| Pro Ser Asn Gly Gln Asp Ile Asn Leu Glu Leu Ser Ile Gly Ile Val | |
| 210 215 220 | |
| tca gct gac tca tct cgg gta tca aat gcc aac tcg gcc gag tcg aaa | 778 |
| Ser Ala Asp Ser Ser Arg Val Ser Asn Ala Asn Ser Ala Glu Ser Lys | |
| 225 230 235 240 | |
| cca aag gta gat aac aac aat ttc cag ttt ctt gaa caa gct atg gtg | 826 |
| Pro Lys Val Asp Asn Asn Asn Phe Gln Phe Leu Glu Gln Ala Met Val | |
| 245 250 255 | |
| gct aag gcg gta tgt ttg tgt tgg caa tta ggt ttt gga aca agt gaa | 874 |
| Ala Lys Ala Val Cys Leu Cys Trp Gln Leu Gly Phe Gly Thr Ser Glu | |
| 260 265 270 | |
| att tgt agg aac tgt caa aat tca aat tca aat ggc ttc tat agt tat | 922 |
| Ile Cys Arg Asn Cys Gln Asn Ser Asn Ser Asn Gly Phe Tyr Ser Tyr | |
| 275 280 285 | |
| tgt aga ccc ttg gat tca tag ggatcatcttt ttcttcttttc tttctgtttt | 973 |
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<213> Gossypium hirsutum

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Gly Glu Gly Cys Trp Arg Ser Leu Pro Lys Ala Ala Gly Leu Leu Arg

35 40 45

Cys Gly Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Pro Asp

50 55 60

Leu Lys Arg Gly Asn Phe Thr Glu Glu Glu Asp Glu Leu Ile Ile Lys
 65 70 75 80
 Leu His Ser Leu Leu Gly Asn Lys Trp Ser Leu Ile Ala Gly Arg Leu
 85 90 95
 Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Asn Thr His Ile
 100 105 110
 Lys Arg Lys Leu Ile Ser Arg Gly Ile Asp Pro Gln Thr His Arg Pro
 115 120 125
 Leu Asn Gln Thr Ala Asn Thr Asn Thr Val Thr Ala Pro Thr Glu Leu
 130 135 140
 Asp Phe Arg Asn Ser Pro Thr Ser Val Ser Lys Ser Ser Ser Ile Lys
 145 150 155 160
 Asn Pro Ser Leu Asp Phe Asn Tyr Asn Glu Phe Gln Phe Lys Ser Asn
 165 170 175
 Thr Asp Ser Leu Glu Glu Pro Asn Cys Thr Ala Ser Ser Gly Met Thr
 180 185 190
 Thr Asp Glu Glu Gln Gln Glu Gln Leu His Lys Lys Gln Gln Tyr Gly
 195 200 205
 Pro Ser Asn Gly Gln Asp Ile Asn Leu Glu Leu Ser Ile Gly Ile Val
 210 215 220
 Ser Ala Asp Ser Ser Arg Val Ser Asn Ala Asn Ser Ala Glu Ser Lys
 225 230 235 240
 Pro Lys Val Asp Asn Asn Asn Phe Gln Phe Leu Glu Gln Ala Met Val
 245 250 255
 Ala Lys Ala Val Cys Leu Cys Trp Gln Leu Gly Phe Gly Thr Ser Glu
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 Met Arg Lys Pro Cys Cys Asp Lys Gln Gly Thr Asn Lys
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 gga gcc tgg tcc aag caa gaa gat caa aag ctc att gat tat ata cgt 158
 Gly Ala Trp Ser Lys Gln Glu Asp Gln Lys Leu Ile Asp Tyr Ile Arg
 15 20 25
 att cat ggt gaa ggc tgt tgg cgt tcc ctc ccc aaa gct gca ggt ttg 206
 Ile His Gly Glu Gly Cys Trp Arg Ser Leu Pro Lys Ala Ala Gly Leu
 30 35 40 45
 cac cgt tgc ggt aaa agt tgc agg ctg aga tgg ata aat tac tta aga 254
 His Arg Cys Gly Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg
 50 55 60

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| cca gat atc aaa cgt ggt aac ttt gct caa gac gaa gag gac tta att | 302 |
| Pro Asp Ile Lys Arg Gly Asn Phe Ala Gln Asp Glu Glu Asp Leu Ile | |
| 65 70 75 | |
| atc aaa ctc cat gct ctc ctt ggt aac cgg tgg tca ctg ata gct ggt | 350 |
| Ile Lys Leu His Ala Leu Leu Gly Asn Arg Trp Ser Leu Ile Ala Gly | |
| 80 85 90 | |
| aga tta cca gga aga aca gat aat gaa gtg aag aac tat tgg aat tcc | 398 |
| Arg Leu Pro Gly Arg Thr Asp Asn Glu Val Lys Asn Tyr Trp Asn Ser | |
| 95 100 105 | |
| cat ata aag aga aag cta atg aag atg ggg atc gat cct aat aac cat | 446 |
| His Ile Lys Arg Lys Leu Met Lys Met Gly Ile Asp Pro Asn Asn His | |
| 110 115 120 125 | |
| aag ttg aac caa tat cct cat cat gtt ggt ccc ctt aac ccc acc acc | 494 |
| Lys Leu Asn Gln Tyr Pro His His Val Gly Pro Leu Asn Pro Thr Thr | |
| 130 135 140 | |
| acc aac tcc atg gat gtg gca tgt aag ctt aga gtg tgt tca aca gac | 542 |
| Thr Asn Ser Met Asp Val Ala Cys Lys Leu Arg Val Cys Ser Thr Asp | |
| 145 150 155 | |
| aat gat gat ggg atc tca gat gct gca agt tat ctc gaa gac gca aca | 590 |
| Asn Asp Asp Gly Ile Ser Asp Ala Ala Ser Tyr Leu Glu Asp Ala Thr | |
| 160 165 170 | |
| ccg ccc act ggt ata tcc aac ttg gac ctt gat ctc aca att gct ttt | 638 |
| Pro Pro Thr Gly Ile Ser Asn Leu Asp Leu Asp Leu Thr Ile Ala Phe | |
| 175 180 185 | |
| cct tcg agt cct atc aag aat att att gaa gaa agc cag cag aaa aca | 686 |
| Pro Ser Ser Pro Ile Lys Asn Ile Ile Glu Glu Ser Gln Gln Lys Thr | |
| 190 195 200 205 | |
| gca tct att gta aca aat gat gaa gaa gaa caa tat aca gtc cct acc | 734 |
| Ala Ser Ile Val Thr Asn Asp Glu Glu Glu Gln Tyr Thr Val Pro Thr | |
| 210 215 220 | |
| ctt ctt ctt ttc aga tga gacaaaaaaaaa aaagcctcac acatgtggag | 782 |
| Leu Leu Leu Phe Arg | |
| 225 | |
| attcgtgcaa aagacctaaa ggcttacgaa ggcaacatgc acgccattgt caaattcttt | 842 |
| tggtatgatgg attgaaacca tctccttgct cattagaaag gaggaagata agctaaaact | 902 |
| gtattattgt gtataaattt ggtagaaaga aagatttcaa cttaagaatt aggatcaaat | 962 |
| aactgaatga atgaacgaat tgcagataag ttgttaggag gttttcaatc aacttatctg | 1022 |
| caattaattt ggtggagctg atgtaggatg atgagttcat cgtacatgaa ctgaaccttt | 1082 |
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 20 25 30
 Glu Gly Cys Trp Arg Ser Leu Pro Lys Ala Ala Gly Leu His Arg Cys
 35 40 45
 Gly Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Pro Asp Ile
 50 55 60
 Lys Arg Gly Asn Phe Ala Gln Asp Glu Glu Asp Leu Ile Ile Lys Leu
 65 70 75 80
 His Ala Leu Leu Gly Asn Arg Trp Ser Leu Ile Ala Gly Arg Leu Pro
 85 90 95
 Gly Arg Thr Asp Asn Glu Val Lys Asn Tyr Trp Asn Ser His Ile Lys
 100 105 110
 Arg Lys Leu Met Lys Met Gly Ile Asp Pro Asn Asn His Lys Leu Asn
 115 120 125
 Gln Tyr Pro His His Val Gly Pro Leu Asn Pro Thr Thr Thr Asn Ser
 130 135 140
 Met Asp Val Ala Cys Lys Leu Arg Val Cys Ser Thr Asp Asn Asp Asp
 145 150 155 160
 Gly Ile Ser Asp Ala Ala Ser Tyr Leu Glu Asp Ala Thr Pro Pro Thr
 165 170 175
 Gly Ile Ser Asn Leu Asp Leu Asp Leu Thr Ile Ala Phe Pro Ser Ser
 180 185 190
 Pro Ile Lys Asn Ile Ile Glu Glu Ser Gln Gln Lys Thr Ala Ser Ile
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 Phe Arg
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 Met Gly Arg Ser Pro Cys Cys Ser Lys
 1 5
 gaa ggc ctt aac aga gga gct tgg act gct ctt gaa gac aaa att ctt 160
 Glu Gly Leu Asn Arg Gly Ala Trp Thr Ala Leu Glu Asp Lys Ile Leu
 10 15 20 25

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| aaa gat tat atc aaa gta cac ggt gaa ggt cgt tgg aga aat ctc ccc | 208 |
| Lys Asp Tyr Ile Lys Val His Gly Glu Gly Arg Trp Arg Asn Leu Pro | |
| 30 35 40 | |
| aaa aga gct ggt ctt aag aga tgt ggg aaa agt tgt agg ctt cgg tgg | 256 |
| Lys Arg Ala Gly Leu Lys Arg Cys Gly Lys Ser Cys Arg Leu Arg Trp | |
| 45 50 55 | |
| ttg aat tat ttg aga cct gat att aaa aga ggt aac ata tca cct gac | 304 |
| Leu Asn Tyr Leu Arg Pro Asp Ile Lys Arg Gly Asn Ile Ser Pro Asp | |
| 60 65 70 | |
| gag gaa gag ctt atc atc aaa ctc cac aaa ctc ttg gga aac aga tgg | 352 |
| Glu Glu Glu Leu Ile Ile Lys Leu His Lys Leu Leu Gly Asn Arg Trp | |
| 75 80 85 | |
| tct ttg ata gct ggg agg ctt cca gga cga aca gac aat gaa ata aag | 400 |
| Ser Leu Ile Ala Gly Arg Leu Pro Gly Arg Thr Asp Asn Glu Ile Lys | |
| 90 95 100 105 | |
| aat tac tgg aac acc aac tta agt aaa aga gtt tcc gat cgt caa aag | 448 |
| Asn Tyr Trp Asn Thr Asn Leu Ser Lys Arg Val Ser Asp Arg Gln Lys | |
| 110 115 120 | |
| tca ccc gcc gct cct tcg aaa aat ccc gag gcg gct cga cga gga act | 496 |
| Ser Pro Ala Ala Pro Ser Lys Asn Pro Glu Ala Ala Arg Arg Gly Thr | |
| 125 130 135 | |
| gct ggt aat ggc aat acc aat ggt aat ggt agt ggt agt tcc tcg aca | 544 |
| Ala Gly Asn Gly Asn Thr Asn Gly Asn Gly Ser Gly Ser Ser Thr | |
| 140 145 150 | |
| cac gtg gtg cgg aca agg gcg aca agg tgc tcc aag gtt ttc ata aac | 592 |
| His Val Val Arg Thr Arg Ala Thr Arg Cys Ser Lys Val Phe Ile Asn | |
| 155 160 165 | |
| cct cct cac tac aca caa aac aga gac cca aag cct tct tca act tgt | 640 |
| Pro Pro His Tyr Thr Gln Asn Arg Asp Pro Lys Pro Ser Ser Thr Cys | |
| 170 175 180 185 | |
| tca aat cat ggg gat cac cgg gaa cct aaa aca atg aat gag ttg tta | 688 |
| Ser Asn His Gly Asp His Arg Glu Pro Lys Thr Met Asn Glu Leu Leu | |
| 190 195 200 | |
| tta ccg ata atg tca gaa tcc gag aat gaa ggg acg acc gat cat ata | 736 |
| Leu Pro Ile Met Ser Glu Ser Glu Asn Glu Gly Thr Thr Asp His Ile | |
| 205 210 215 | |
| tca tcg gat ttt aca ttt gac ttc aac atg gga gag ttt tgt tta tcg | 784 |
| Ser Ser Asp Phe Thr Phe Asp Phe Asn Met Gly Glu Phe Cys Leu Ser | |
| 220 225 230 | |
| gat ctt ttg aat tcc gat ttc tgc gat gta aac gag ctt aat tac agc | 832 |
| Asp Leu Leu Asn Ser Asp Phe Cys Asp Val Asn Glu Leu Asn Tyr Ser | |
| 235 240 245 | |
| aat ggt ttt gat tcg tca ccc tca ccg gat cag cct cct atg gat ttc | 880 |
| Asn Gly Phe Asp Ser Ser Pro Ser Pro Asp Gln Pro Pro Met Asp Phe | |
| 250 255 260 265 | |

tcc gac gaa atg cta aaa gag tgg acg gcc gcc gcc tcc act cac tgc 928
 Ser Asp Glu Met Leu Lys Glu Trp Thr Ala Ala Ala Ser Thr His Cys
 270 275 280

tgt cac caa agt gcg gct tcc aat ctc cag tcc ttg cct cca ttt att 976
 Cys His Gln Ser Ala Ala Ser Asn Leu Gln Ser Leu Pro Pro Phe Ile
 285 290 295

gaa aat gga att gaa tga ccttgaaaaa ataaaagacg aaaaatattt 1024
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 <213> Gossypium hirsutum

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 35 40 45
 Cys Gly Lys Ser Cys Arg Leu Arg Trp Leu Asn Tyr Leu Arg Pro Asp
 50 55 60
 Ile Lys Arg Gly Asn Ile Ser Pro Asp Glu Glu Leu Ile Ile Lys
 65 70 75 80
 Leu His Lys Leu Leu Gly Asn Arg Trp Ser Leu Ile Ala Gly Arg Leu
 85 90 95
 Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Asn Thr Asn Leu
 100 105 110
 Ser Lys Arg Val Ser Asp Arg Gln Lys Ser Pro Ala Ala Pro Ser Lys
 115 120 125
 Asn Pro Glu Ala Ala Arg Arg Gly Thr Ala Gly Asn Gly Asn Thr Asn
 130 135 140
 Gly Asn Gly Ser Gly Ser Ser Ser Thr His Val Val Arg Thr Arg Ala
 145 150 155 160
 Thr Arg Cys Ser Lys Val Phe Ile Asn Pro Pro His Tyr Thr Gln Asn
 165 170 175
 Arg Asp Pro Lys Pro Ser Ser Thr Cys Ser Asn His Gly Asp His Arg
 180 185 190
 Glu Pro Lys Thr Met Asn Glu Leu Leu Leu Pro Ile Met Ser Glu Ser
 195 200 205
 Glu Asn Glu Gly Thr Thr Asp His Ile Ser Ser Asp Phe Thr Phe Asp
 210 215 220
 Phe Asn Met Gly Glu Phe Cys Leu Ser Asp Leu Leu Asn Ser Asp Phe
 225 230 235 240
 Cys Asp Val Asn Glu Leu Asn Tyr Ser Asn Gly Phe Asp Ser Ser Pro
 245 250 255
 Ser Pro Asp Gln Pro Pro Met Asp Phe Ser Asp Glu Met Leu Lys Glu
 260 265 270
 Trp Thr Ala Ala Ala Ser Thr His Cys Cys His Gln Ser Ala Ala Ser
 275 280 285
 Asn Leu Gln Ser Leu Pro Pro Phe Ile Glu Asn Gly Ile Glu
 290 295 300

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| cg | gc | ac | gaga | ct | cca | aaca | atg | tcc | atg | aaa | aaa | gaa | ggt | gaa | att | cta | 112 |
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| aaa | aag | gga | tta | tgg | gca | atg | gag | gaa | gac | aag | tta | ctc | att | gat | tat | | 160 |
| Lys | Lys | Gly | Leu | Trp | Ala | Met | Glu | Glu | Asp | Lys | Leu | Leu | Ile | Asp | Tyr | | |
| | | | 15 | | | | | 20 | | | | | 25 | | | | |
| gtc | aat | gtc | cat | gga | aaa | gga | caa | tgg | aac | aaa | ata | gcc | aac | aga | aca | | 208 |
| Val | Asn | Val | His | Gly | Lys | Gly | Gln | Trp | Asn | Lys | Ile | Ala | Asn | Arg | Thr | | |
| | | | 30 | | | | 35 | | | | | 40 | | | | | |
| ggt | ttg | aag | aga | agt | ggg | aaa | agt | tgt | cgg | cta | agg | tgg | atg | aat | tac | | 256 |
| Gly | Leu | Lys | Arg | Ser | Gly | Lys | Ser | Cys | Arg | Leu | Arg | Trp | Met | Asn | Tyr | | |
| | 45 | | | | | 50 | | | | | 55 | | | | | | |
| ctg | agt | cct | aac | gtt | aaa | aag | ggt | gat | ttt | tct | gaa | gaa | gaa | gaa | gac | | 304 |
| Leu | Ser | Pro | Asn | Val | Lys | Lys | Gly | Asp | Phe | Ser | Glu | Glu | Glu | Glu | Asp | | |
| | 60 | | | | 65 | | | | 70 | | | | | | 75 | | |
| ctc | gtc | att | aga | ctt | cat | aag | ctt | ctt | gga | aac | agg | tgg | tct | ttg | att | | 352 |
| Leu | Val | Ile | Arg | Leu | His | Lys | Leu | Leu | Gly | Asn | Arg | Trp | Ser | Leu | Ile | | |
| | | | | 80 | | | | | 85 | | | | | 90 | | | |
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| Ala | Lys | Arg | Val | Pro | Gly | Arg | Thr | Asp | Asn | Gln | Val | Lys | Asn | Tyr | Trp | | |
| | | | 95 | | | | | 100 | | | | | 105 | | | | |
| aat | agt | cat | ttg | agg | aag | aaa | cta | ggg | atc | att | gat | caa | aac | aag | aca | | 448 |
| Asn | Ser | His | Leu | Arg | Lys | Lys | Leu | Gly | Ile | Ile | Asp | Gln | Asn | Lys | Thr | | |
| | | | 110 | | | | 115 | | | | | 120 | | | | | |
| agg | atc | gat | ttt | tgt | caa | agt | tca | aag | caa | gtc | aaa | gtg | tgt | cat | gtt | | 496 |
| Arg | Ile | Asp | Phe | Cys | Gln | Ser | Ser | Lys | Gln | Val | Lys | Val | Cys | His | Val | | |
| | 125 | | | | | 130 | | | | | 135 | | | | | | |

gat gag gca gcc acg gat cca agt cct gga cat gga aca acc act gaa 544
Asp Glu Ala Ala Thr Asp Pro Ser Pro Gly His Gly Thr Thr Thr Glu
140 145 150 155

acc acg ggt ata aca gtg gat cag agt aac cag cag gaa gtc att gat 592
Thr Thr Gly Ile Thr Val Asp Gln Ser Asn Gln Gln Glu Val Ile Asp
160 165 170

cat cgg gtc tta aac aat act act caa gaa tca atg acc agt gag agt 640
His Arg Val Leu Asn Asn Thr Thr Gln Glu Ser Met Thr Ser Glu Ser
175 180 185

tat atc aac act ttc tgg att cct gac cat gat tat gag cta agt aca 688
Tyr Ile Asn Thr Phe Trp Ile Pro Asp His Asp Tyr Glu Leu Ser Thr
190 195 200

ctt gcc atg att gac cat gat tat gag cta agt aca ctt gcc atg att 736
Leu Ala Met Ile Asp His Asp Tyr Glu Leu Ser Thr Leu Ala Met Ile
205 210 215

gac cac ttc cat gaa tgt tct tct ttt cat ctt agc tag agactatggt 785
Asp His Phe His Glu Cys Ser Ser Phe His Leu Ser
220 225 230

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20 25 30
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35 40 45
Gly Lys Ser Cys Arg Leu Arg Trp Met Asn Tyr Leu Ser Pro Asn Val
50 55 60
Lys Lys Gly Asp Phe Ser Glu Glu Glu Glu Asp Leu Val Ile Arg Leu
65 70 75 80
His Lys Leu Leu Gly Asn Arg Trp Ser Leu Ile Ala Lys Arg Val Pro
85 90 95
Gly Arg Thr Asp Asn Gln Val Lys Asn Tyr Trp Asn Ser His Leu Arg
100 105 110
Lys Lys Leu Gly Ile Ile Asp Gln Asn Lys Thr Arg Ile Asp Phe Cys
115 120 125
Gln Ser Ser Lys Gln Val Lys Val Cys His Val Asp Glu Ala Ala Thr
130 135 140
Asp Pro Ser Pro Gly His Gly Thr Thr Thr Glu Thr Thr Gly Ile Thr
145 150 155 160
Val Asp Gln Ser Asn Gln Gln Glu Val Ile Asp His Arg Val Leu Asn
165 170 175
Asn Thr Thr Gln Glu Ser Met Thr Ser Glu Ser Tyr Ile Asn Thr Phe
180 185 190

Trp Ile Pro Asp His Asp Tyr Glu Leu Ser Thr Leu Ala Met Ile Asp
195 200 205
His Asp Tyr Glu Leu Ser Thr Leu Ala Met Ile Asp His Phe His Glu
210 215 220
Cys Ser Ser Phe His Leu Ser
225 230

<210> 9
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<223> Description of Artificial Sequence:degenerate
'universal' MYB primer

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<212> DNA
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<220>
<223> Description of Artificial Sequence:degenerate
'universal' MYB primer

<220>
<221> modified_base
<222> (17)
<223> n = g, a, c or t

<400> 10
srttrtctgt tckkccngg

19

<210> 11
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:highly
conserved peptide coded by degenerate 'universal'
MYB primer

<400> 11
Gly Lys Ser Cys Arg Leu
1 5

<210> 12
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:highly
conserved peptide coded by degenerate 'universal'
MYB primer

<400> 12
Pro Gly Arg Thr Asp Asn
1 5

<210> 13
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:oligonucleotide
primer COT105

<400> 13
aagcagagga attgatccac 20

<210> 14
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:oligonucleotide
primer COT106

<400> 14
accctatgaa tccaagggtc 20

<210> 15
<211> 19
<212> DNA
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<220>
<223> Description of Artificial Sequence:oligonucleotide
primer COT107

<400> 15
cctcggaaca aattgtgcc 19

<210> 16
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:oligonucleotide
primer COT108

<400> 16
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19

<210> 17
<211> 20
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<220>
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primer COT109

<400> 17
cagaaggaga aacacagagg

20

<210> 18
<211> 20
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<220>
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primer COT110

<400> 18
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20

<210> 19
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:oligonucleotide
primer COT111

<400> 19
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20

<210> 20
<211> 20
<212> DNA
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<220>
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primer COT112

<400> 20
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<210> 21
 <211> 20
 <212> DNA
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<220>
 <223> Description of Artificial Sequence:oligonucleotide
 primer COT113

<400> 21
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<210> 22
 <211> 20
 <212> DNA
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<220>
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 primer COT114

<400> 22
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<210> 23
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:oligonucleotide
 primer COT115

<400> 23
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<210> 24
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:oligonucleotide
 primer COT116

<400> 24
 acaatggcgt gcatgttgcc 20

<210> 25
 <211> 7
 <212> PRT
 <213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence:conserved motif
      within the basic 'transregulatory region 1' (TRR1)
      domain

<220>
<221> MOD_RES
<222> (5)..(6)
<223> Xaa = any amino acid

<400> 25
Gly Ile Asp Pro Xaa Xaa His
 1             5

<210> 26
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:cysteine-rich
      zinc-finger motif

<220>
<221> MOD_RES
<222> (2)
<223> Xaa = any amino acid

<220>
<221> MOD_RES
<222> (4)..(13)
<223> Xaa = any amino acid

<220>
<221> MOD_RES
<222> (15)..(16)
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<400> 26
Cys Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa
 1             5             10             15
Cys

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